



IFWO

RAW SEQUENCE LISTING

DATE: 09/17/2004

PATENT APPLICATION: US/10/824,131

TIME: 09:05:07

Input Set : N:\Crf3\RULE60\10824131.raw.txt

Output Set: N:\CRF4\09172004\J824131.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Palmer, Leslie M.

7 (ii) TITLE OF INVENTION: Novel ribG

10 (iii) NUMBER OF SEQUENCES: 7

12 (iv) CORRESPONDENCE ADDRESS:

13 (A) ADDRESSEE: Dechert Price & Rhoads

14 (B) STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre

15 (C) CITY: Philadelphia

16 (D) STATE: PA

17 (E) COUNTRY: US

18 (F) ZIP: 19103

20 (v) COMPUTER READABLE FORM:

21 (A) MEDIUM TYPE: Diskette

22 (B) COMPUTER: IBM Compatible

23 (C) OPERATING SYSTEM: DOS

24 (D) SOFTWARE: FastSEQ for Windows Version 2.0

26 (vi) CURRENT APPLICATION DATA:

C--> 27 (A) APPLICATION NUMBER: US/10/824,131

C--> 28 (B) FILING DATE: 14-Apr-2004

29 (C) CLASSIFICATION:

31 (vii) PRIOR APPLICATION DATA:

W--> 32 (A) APPLICATION NUMBER: US/09/376,633

33 (B) FILING DATE: 1999-August-18

W--> 34 (A) APPLICATION NUMBER: 08/978,456

35 (B) FILING DATE:

39 (viii) ATTORNEY/AGENT INFORMATION:

40 (A) NAME: Dickinson, Todd Q

41 (B) REGISTRATION NUMBER: 28,354

42 (C) REFERENCE/DOCKET NUMBER: P50444-9

44 (ix) TELECOMMUNICATION INFORMATION:

45 (A) TELEPHONE: 215-994-2252

46 (B) TELEFAX: 215-994-2222

47 (C) TELEX:

50 (2) INFORMATION FOR SEQ ID NO: 1:

52 (i) SEQUENCE CHARACTERISTICS:

53 (A) LENGTH: 1029 base pairs

54 (B) TYPE: nucleic acid

55 (C) STRANDEDNESS: double

56 (D) TOPOLOGY: linear

59 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

61 ATGGATTATG CGATTCAACT TGCAAATATG GTACAAGGTC AAACAGGTGT TAATCCACCC 60

62 GTTGGCGCTG TTGTAGTTAA TGAAGGTAGG ATTGTTGGTA TTGGTGCACA CTTGAGAAAA 120

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63  GGTGACAAGC ATGCGGAGGT TCAAGCACTT GATATGGCAC AACAAAATGC TGAAGGTGCG      180
64  ACGATTTATA TTACGTTAGA GCCATGTAGT CATTTTGGTT CAACACCACC CTGTGTTAAC      240
65  AAAATTATTG ATTGTAAGAT AGCAAAAGTA GTATACGCAA CAAAAGACAA TTCGTTAGAC      300
66  ACACATGGTG ATGAGACGTT ACGGGCTCAC GGTATTGAGG TTGAATGCGT TGATGATGAA      360
67  CGGGCATCAC AATTATACCA AGACTTTTTT AAAGCAAAAG CAAAGCAACT GCCACAAATT      420
68  ACAGTGAAAG TATCTGCAAG TTTAGATGGT AAACAAGCGA ATGATAATGG ACAAAGTCAA      480
69  TGGATTACTA ACAAAGAGGT TAAACAAGAT GTCTATAAGT TAAGACATCG ACACGACGCA      540
70  GTGTAACTG GAAGACGTAC AGTTGAATTA GATGATCCAC AATATACTAC ACGTATTCAA      600
71  GATGGAAAAA ACCCTATAAA AGTAATATTG TCTAAGTCTG GGAATATTCA TTTTAATCAG      660
72  CAAATTTATC AAGATGAATC AACACCAATT TGGATATATA CTGAAAATCC AAATTTAACA      720
73  AGCAATCAAA CACATATTGA AATTATTTAC TTGAAGTCTT GTGATTTAAC AACAAATCTT      780
74  CACAATTTAT ATAAAAGAGG AGTTGGAAGT TTGCTAGTCG AGGCAGGTCC AACCCTACT      840
75  TCAGAATTCT CCATCTATTA TATAGATGAA TTTATTCTCT ATTATGCCCC GAAATTAATT      900
76  GGCGGATCTG GAAATTATCA ATTTTATCAA ACAAATGATG TGATTGAGAT ACCAGATGCG      960
77  AACCAATTTG AAATTGTTCA TTCCGAGTTA TTAAATCAAA ATGTTAAATT AACTTTACGA     1020
78  AAGAAGTGA                                         1029

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(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 342 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

91  Met Asp Tyr Ala Ile Gln Leu Ala Asn Met Val Gln Gly Gln Thr Gly
92  1          5          10          15
93  Val Asn Pro Pro Val Gly Ala Val Val Val Asn Glu Gly Arg Ile Val
94          20          25          30
95  Gly Ile Gly Ala His Leu Arg Lys Gly Asp Lys His Ala Glu Val Gln
96          35          40          45
97  Ala Leu Asp Met Ala Gln Gln Asn Ala Glu Gly Ala Thr Ile Tyr Ile
98          50          55          60
99  Thr Leu Glu Pro Cys Ser His Phe Gly Ser Thr Pro Pro Cys Val Asn
100  65          70          75          80
101  Lys Ile Ile Asp Cys Lys Ile Ala Lys Val Val Tyr Ala Thr Lys Asp
102          85          90          95
103  Asn Ser Leu Asp Thr His Gly Asp Glu Thr Leu Arg Ala His Gly Ile
104          100          105          110
105  Glu Val Glu Cys Val Asp Asp Glu Arg Ala Ser Gln Leu Tyr Gln Asp
106          115          120          125
107  Phe Phe Lys Ala Lys Ala Lys Gln Leu Pro Gln Ile Thr Val Lys Val
108          130          135          140
109  Ser Ala Ser Leu Asp Gly Lys Gln Ala Asn Asp Asn Gly Gln Ser Gln
110          145          150          155          160
111  Trp Ile Thr Asn Lys Glu Val Lys Gln Asp Val Tyr Lys Leu Arg His
112          165          170          175
113  Arg His Asp Ala Val Leu Thr Gly Arg Arg Thr Val Glu Leu Asp Asp
114          180          185          190
115  Pro Gln Tyr Thr Thr Arg Ile Gln Asp Gly Lys Asn Pro Ile Lys Val
116          195          200          205

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```

117 Ile Leu Ser Lys Ser Gly Asn Ile His Phe Asn Gln Gln Ile Tyr Gln
118      210                      215                      220
119 Asp Glu Ser Thr Pro Ile Trp Ile Tyr Thr Glu Asn Pro Asn Leu Thr
120      225                      230                      235                      240
121 Ser Asn Gln Thr His Ile Glu Ile Ile Tyr Leu Lys Ser Cys Asp Leu
122                      245                      250                      255
123 Thr Thr Ile Leu His Asn Leu Tyr Lys Arg Gly Val Gly Thr Leu Leu
124                      260                      265                      270
125 Val Glu Ala Gly Pro Thr Thr Thr Ser Glu Phe Ser Ile Tyr Tyr Ile
126                      275                      280                      285
127 Asp Glu Phe Ile Leu Tyr Tyr Ala Pro Lys Leu Ile Gly Gly Ser Gly
128                      290                      295                      300
129 Asn Tyr Gln Phe Tyr Gln Thr Asn Asp Val Ile Glu Ile Pro Asp Ala
130      305                      310                      315                      320
131 Asn Gln Phe Glu Ile Val His Ser Glu Leu Leu Asn Gln Asn Val Lys
132                      325                      330                      335
133 Leu Thr Leu Arg Lys Lys
134                      340

```

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1269 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```

147 AANCACCAAT CCNATTGGGA GGNAATCCAA ATCAATNCCC GGANNCCCAA TCCAAGTTAA      60
148 TTAAGTCCAA GGTTTTGGAA CATTACCAAA TATGATTCCG ATGAGGTCAA ATGNCAANCG      120
149 GTGTTAATAA ACTACGAAAT GNTGTGNAAA TGATAGTAGA NCAAGTTGCG CATACAGTNT      180
150 CTCNATTATA TGATGCTTTA GAATCGAATG AGCAACAACA GCGCAGTTAC AATCAATAAT      240
151 TTGTAAGTAG AAGATAATAA AGAGAACGCT CTATAGAGAC GAATTGAAGG TTTGATTTTA      300
152 ATGTCTGTGA GTAAGAATCA TATCAATGAG ATGCCTATAG TACTCAGATT ATATTAAATT      360
153 AAAACCGTCA TTAATTGTTT TTTTAGAAAA CATATAGTAT CATTTTAAAT GTAGTTGACA      420
154 TACTACGTAC TCAAATAATC TATAACAATT TCATATATAA TTCTTTCGGG GCAGGGTGAA      480
155 ATTCCCAACC GGCAGTAAAT AAAGCCTGCG ACCTGCTAAT ATGTTTCATA TTAGTGGCTG      540
156 ATCTAGTGAG ATTCTAGAGC CGACAGTTAA AGTCTGGATG GGAGAAAGAA TGTTAATTAT      600
157 CGACAAAGAT AATGTAGCGT ATTTGTAAAA ATGTGTACAA ATAGGCTTAT TTAACGATAA      660
158 ATTTTCTCC TTTGCATCTT AATTCATGAT GTGAGGATTT TTTGTTTATA GAGGTGATCA      720
159 TTTGAGTCAA TTTATGGATT ATGCGATTCA ACTTCCAAAT ATGGTACAAG GTCANACAGG      780
160 TGTTAATCCA CCCGTTGGCG CTGTTGTAGT TAATGAAGGT AGGATTGTTG GTATTGGTGC      840
161 ACACTTGAGA AAAGGTGACA AGCATGCGGA GGTTCAAGCA CTTGATATGG CACAACANAA      900
162 TGCTGAAGGT GCGACGATTT ATATTACGTT AGAGCCATGT AGTCATTTTG GTTCAACACC      960
163 ACCCTGTGTT AACAAAATTA TTGATTGTAA GATAGCANAA GTAGTATTAC NCAACANAAG      1020
164 ACAATTCGGT TAGACACACA TGGGTGATGA GACGTTACGG GGCTCCACGG TATTTGAGGG      1080
165 TTGAATTGCG TTGGATGATG AACGGGCATC ACAATTATAC CAAAGACTTT TTTTAAAGCA      1140
166 AAAAGCAAAG CAACTTGCCA CAAATTACA GTGAAAGTNT CTTGAAAGTT TAGATGGGTA      1200
167 AACAAAGCGA ATTGATAATG GACAAAGTCA ATGGATTACT AACAAAGAGG TTAAACAAGA      1260
168 TGTCTATAG                                     1269

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(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

RAW SEQUENCE LISTING

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Input Set : N:\Crif3\RULE60\10824131.raw.txt

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173          (A) LENGTH: 99 amino acids
174          (B) TYPE: amino acid
175          (C) STRANDEDNESS: single
176          (D) TOPOLOGY: linear
179      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
W--> 181  Met Asp Tyr Ala Ile Gln Leu Pro Asn Met Val Gln Gly Xaa Thr Gly
182      1          5          10          15
183  Val Asn Pro Pro Val Gly Ala Val Val Val Asn Glu Gly Arg Ile Val
184      20          25          30
185  Gly Ile Gly Ala His Leu Arg Lys Gly Asp Lys His Ala Glu Val Gln
186      35          40          45
187  Ala Leu Asp Met Ala Gln Xaa Asn Ala Glu Gly Ala Thr Ile Tyr Ile
188      50          55          60
189  Thr Leu Glu Pro Cys Ser His Phe Gly Ser Thr Pro Pro Cys Val Asn
190      65          70          75          80
191  Lys Ile Ile Asp Cys Lys Ile Ala Xaa Val Val Leu Xaa Asn Xaa Arg
192      85          90          95
193  Gln Phe Arg
196  (2) INFORMATION FOR SEQ ID NO: 5:
198      (i) SEQUENCE CHARACTERISTICS:
199          (A) LENGTH: 21 base pairs
200          (B) TYPE: nucleic acid
201          (C) STRANDEDNESS: single
202          (D) TOPOLOGY: linear
205      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
207  ATGAAGGTAG GATTGTTGGT A
209  (2) INFORMATION FOR SEQ ID NO: 6:
211      (i) SEQUENCE CHARACTERISTICS:
212          (A) LENGTH: 22 base pairs
213          (B) TYPE: nucleic acid
214          (C) STRANDEDNESS: single
215          (D) TOPOLOGY: linear
218      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
220  AGTCTTG GTA TAATTGTGAT GC
222  (2) INFORMATION FOR SEQ ID NO: 7:
224      (i) SEQUENCE CHARACTERISTICS:
225          (A) LENGTH: 3336 base pairs
226          (B) TYPE: nucleic acid
227          (C) STRANDEDNESS: double
228          (D) TOPOLOGY: linear
231      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
233  ATGGATTATG CGATTCAACT TGCAAATATG GTACAAGGTC AAACAGGTGT TAATCCACCC 60
234  GTTGGCGCTG TTGTAGTTAA TGAAGGTAGG ATTGTTGGTA TTGGTGCACA CTTGAGAAAA 120
235  GGTGACAAGC ATGCGGAGGT TCAAGCACTT GATATGGCAC AACAAAATGC TGAAGGTGCG 180
236  ACGATTTATA TTACGTTAGA GCCATGTAGT CATTTTGGTT CAACACCACC CTGTGTTAAC 240
237  AAAATTATTG ATTGTAAGAT AGCAAAAAGTA GTATACGCAA CAAAAGACAA TTCGTTAGAC 300
238  ACACATGGTG ATGAGACGTT ACGGGCTCAC GGTATTGAGG TTGAATGCGT TGATGATGAA 360
239  CGGGCATCAC AATTATACCA AGACTTTTTT AAAGCAAAAG CAAAGCAACT GCCACAAATT 420
240  ACAGTGAAAG TATCTGCAAG TTTAGATGGT AAACAAGCGA ATGATAATGG ACAAAGTCAA 480

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241	TGGATTACTA	ACAAAGAGGT	TAAACAAGAT	GTCTATAAGT	TAAGACATCG	ACACGACGCA	540
242	GTGTAACTG	GAAGACGTAC	AGTTGAATTA	GATGATCCAC	AATATACTAC	ACGTATTCAA	600
243	GATGGAAAAA	ACCCTATAAA	AGTAATATTG	TCTAAGTCTG	GGAATATTCA	TTTAAATCAG	660
244	CAAAATTTATC	AAGATGAATC	AACACCAATT	TGGATATATA	CTGAAAATCC	AAATTTAACA	720
245	AGCAATCAAA	CACATATTGA	AATTATTTAC	TTGAAGTCTT	GTGATTTAAC	AACAATTCTT	780
246	CACAATTTAT	ATAAAAGAGG	AGTTGGAACT	TTGCTAGTCG	AGGCAGGTCC	AACCACTACT	840
247	TCAGAATTCT	CCATCTATTA	TATAGATGAA	TTTATTCTCT	ATTATGCCCC	GAAATTAATT	900
248	GGCGGATCTG	GAAATTATCA	ATTTTATCAA	ACAAATGATG	TGATTGAGAT	ACCAGATGCG	960
249	AACCAATTTG	AAATTGTTCA	TTCCGAGTTA	TTAAATCAAA	ATGTTAAATT	AACTTTACGA	1020
250	AAGAAGTGAT	GATGCATGTT	TACTGGCATC	GTTGAAGAAA	TAGGTGTCGT	TAAAAGTGTT	1080
251	CAAATTCGTC	AATCAGTCAG	GACGATTGAA	ATCGAAGCAC	ATAAGATTAC	GGCAGATATG	1140
252	CATATTGGTG	ATTCCATCAG	TGTTAATGGT	GCATGTTTAA	CAGTGATTGA	TTTTGATCAG	1200
253	ACATCTTTTA	CTGTTCAAGT	AATTA AAAAGC	ACTGAAAATA	AAACCTATTT	AGCAGATGTT	1260
254	AAGCGACAAT	CAGAAGTAAA	TTTAGAGCGT	GCCATGAGTG	GTAACGGTAG	GTTTGGTGGA	1320
255	CATTTTGTCC	TCGGTCATGT	AGATGAACTA	GGAACAGTTT	CAAAAATAAA	TGAAACAGCC	1380
256	AATGCCAAAA	TTATTACGAT	TCAATGTAGC	CAACATATTA	ATAATCAGTT	AGTTAAGCAA	1440
257	GGGTCTATTA	CTGTGGATGG	TGTAAGTCTA	ACGGTATTTG	ATAAGCATGA	TAACAGTTTT	1500
258	GACATTCATC	TTATTCCAGA	AACGAGGCGT	TCAACGATTT	TATCATCCAA	AAAATTAGGA	1560
259	GATAAAGTAC	ATTTAGAAAC	AGACGTTTTG	TTTAAATATG	TTGAAAATAT	TTTAAATAAA	1620
260	GATAAAGACC	AATTATCTGT	AGATAAATTA	AGAGCATTTG	GTTTTTAGGA	GGGGTAGCAT	1680
261	GCAATTCGAT	AATATTGACA	GTGCTTTAAT	AGCTTTAAAA	AATGGAGAAA	CAATTATTGT	1740
262	AGTAGATGAT	GAGAATCGTG	AAAATGAAGG	TGATTTAGTA	GCGGTTACTG	AATGGATGAA	1800
263	CGATAATACC	ATTAATTTTA	TGGCGAAAGA	AGCAAGGGGA	TTAATATGCG	CACCAGTGTC	1860
264	TAAAGATATT	GCACAACGTT	TGGATTTGGT	ACAAATGGTT	GATGATAACT	CCGACATCTT	1920
265	TGGTACGCAA	TTTACAGTGA	GTATTGATCA	TGTAGATACA	ACAACAGGAA	TTAGTGCTTA	1980
266	TGAACGTACA	TTGACTGCCA	AAAAGCTCAT	TGATCCTAGT	AGTGAAGCTA	AAGATTTTAA	2040
267	TCGTCTGGT	CATTTATTTT	CATTAGTAGC	ACAAGATAAA	GGCGTATTAG	CTAGAAATGG	2100
268	ACACACAGAA	GCGGCTGTTG	ATTTAGCTAA	ACTTACTGGT	GCCAAGCCCG	CTGGTGTCAT	2160
269	TTGTGAGATT	ATGAATGATG	ACGGCACGAT	GGCGAAAGGA	CAAGATTTAC	AAAATTTTAA	2220
270	AGAAAAACAT	CAATTAAAGA	TGATTACGAT	TGATGATTTA	ATTGAATATC	GTAAAAAATT	2280
271	AGAACCAGAA	ATTGAATTTA	AGGCAAAAGT	GAAAATGCCT	ACAGATTTTC	GAACATTTGA	2340
272	TATGTATGGT	TTTAAAGCGA	CATACACAGA	TGAAGAGATA	GTTGTACTGA	CAAAAGGTGC	2400
273	AATTCGACAA	CATGAAAATG	TACGCTTACA	TTCTGCGTGC	CTTACAGGCG	ATATTTTCCA	2460
274	TAGTCAACGT	TGTGATTGTG	GTGCTCAACT	TGAATCGTCT	ATGAAGTATA	TCAATGAACA	2520
275	TGGTGGCATG	ATTATTTATC	TACCTCAAGA	AGGTCGTGGC	ATAGGATTGT	TAAACAAATT	2580
276	ACGCGCATAT	GAATTAATTG	AGCAAGGATA	TGATACAGTA	ACTGCAAATT	TAGCATTAGG	2640
277	TTTTGATGAA	GATTTACGAG	ATTATCATAT	TGCTGCACAG	ATTTTAAAAAT	ATTTTAACAT	2700
278	CGAACATATC	AATTTATTAA	GTAATAATCC	AAGTAAATTT	GAGGGATTAA	AACAATATGG	2760
279	CATTGATATT	GCAGAAAGAA	TTGAAGTTAT	CGTACCAGAA	ACGGTACATA	ATCATGATTA	2820
280	TATGGTAACG	AAAAAAATAA	AAATGGGTCA	TTTAATATAG	GAGGACTTTA	ACATGAATTT	2880
281	TGAAGGTAAA	TTAATTGGAA	AAGATTTGAA	AGTTGCAATC	GTAGTTAGTC	GATTTAATGA	2940
282	TTTTATCACT	GGAAGATTAC	TTGAAGGTGC	AAAAGATACT	TTGATTTCGAC	ATGATGTTAA	3000
283	TGAAGACAAT	ATTGATGTAG	CATTTGTTCC	TGGTGCGTTT	GAAATTCCTT	TAGTAGCTAA	3060
284	AAAATTAGCC	TCATCAGGAA	ATTATGATGC	AATAATTACA	TTAGGATGCG	TAATTCGCGG	3120
285	TGCTACGTCT	CATTATGATT	ATGTTTGTA	TGAAGTGC	AAGGTGTTTC	TAAAGTAAAT	3180
286	GATCAAATA	ATGTACCAGT	CATATTTGGT	ATTTTAACGA	CTGAAAGTAT	TGAACAAGCT	3240
287	GTGGAAGAG	CAGGTACGAA	AGCTGGTAAT	AAAGGTGCCG	AAGCAGCAGT	AAGTGCAATT	3300
288	GAAATGGCTA	ATTTATTAAA	ATCTATAAAA	GCATAG			3336

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 3,13,23,37,44,45,114,118,142,147,161,179,184,775,898,998

Seq#:3; N Pos. 1011,1017,1179

Seq#:4; Xaa Pos.14,55,89,93,95

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/824,131

DATE: 09/17/2004

TIME: 09:05:09

Input Set : N:\Crf3\RULE60\10824131.raw.txt

Output Set: N:\CRF4\09172004\J824131.raw

L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:34 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1) (vii)

L:181 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0

M:341 Repeated in SeqNo=4